

GenCore version 5.1.3
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 OM protein - protein search, using sw model

Run on: November 7, 2002, 10:03:04 : Search time 27.277 Seconds
 (without alignments)
 4034.242 Million cell updates/sec

Title: US-09-125-005-6
 Perfect score: 33848
 Sequence: 1 MAQSTATSPGGTPEHMS.....PDGKARKQPIKEETBAEH 636
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 562222 seqs, 172994929 residues
 Total number of hits satisfying chosen parameters: 562222
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Database : SPREMBL_19:
 1: sp_archaea:*

2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phage:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_rvirus:*
 16: sp_bacteriaph:*
 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3014.5	69.1	631	Q9JJP2	mus musculu
2	2830.5	83.6	590	Q9JJP1	mus musculu
3	2807.5	74.1	514	Q9CUT7	mus musculu
4	2114.5	71.4	641	Q9w664	barbus barb
5	2379	70.3	497	Q9WUJ0	mus musculu
6	1790	52.9	641	Q9UP28	homo sapien
7	1790	52.9	680	Q9H3D4	homo sapien
8	1789	52.9	663	Q9JJE3	rattus norvegicus
9	1789	52.9	680	Q98898	mus musculu
10	1789	52.9	680	Q9JJP6	rattus norvegicus
11	1786	52.8	641	Q75195	homo sapien
12	1782	52.7	680	Q9E010	homo sapien
13	1743	51.5	596	Q98097	mus musculu
14	1741	51.4	586	Q9UBV9	homo sapien
15	1740	51.4	586	Q9JJE2	rattus norvegicus
16	1737	51.3	586	Q9PIB4	homo sapien

ALIGNMENTS

RESULT 1	Q9JJP2	PRELIMINARY;	PRT;	631 AA.
	ID Q9JJP2;			
	AC Q9JJP2;			
	DT 01-OCT-2000 (REMBUREL 15; Created), 01-OCT-2000 (REMBUREL 15; Last sequence update)			
	DT 01-DEC-2001 (REMBUREL 19; Last annotation update)			
	DE P73 ALPHA PROTEIN.			
	GN TRP73 OR P73.			
	OS Mus musculus (Mouse).			
	OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	NCBI TAXID=1090;			
	RN [1]			
	RP SEQUENCE FROM N.A. MEDLINE=2017945; PubMed=10716451; RA Yang A., Walker N., Bronson R., Kaghad M., Bonnin J., Vagner C., Bonnet H., Dikkes P., Sharpe A., McKeon F., Caput D.; RT P73-deficient mice have neurological, pheromonal and inflammatory defects but lack spontaneous tumors.			
	RL Nature 404:99-103(2000).			
	DR EMBL; Y19234; CAB81953.1; DR HSSP; O1550; ICOK.			
	DR MGII:MGII-133691; Trp73.			
	DR InterPro; IPR002117; P53.			
	DR InterPro; IPR001660; SAM.			
	DR Pfam; PF00870; P53; 1.			
	DR Pfam; PF00536; SAM; 1.			
	DR PRINTS; PRO0366; P53SUPPRESSR.			
	DR SMART; SM00454; SAM; 1.			
	DR PROSITE; PS00348; P53; UNKNOWN_1.			
	SQ SEQUENCE 631 AA; 69095 MW; E364D566A90CBF1D CRC64;			
	Query Match 89.1%; Score 3014.5; DB 11; Length 631; Best Local Similarity 88.8%; Pred. No. 3.6e-15; Gaps 6; Matches 569; Conservative 25; Mismatches 32; Indels 15;			

Db	1	WQPHIFEVYEQSSSTPEHLNSLEPDTIFDLPSPGTSEAPSSEASQSEESNMDYFLQG-----	53	DR PRODom; P002681; P53; 1.
DR		DR SMART; SM00454; SAM; 1.		DR PROSITE; PS00348; P53; UNKNOWN_1.
DR		DR PROSITE; PS00348; P53; UNKNOWN_1.		DR PROSITE; PS00348; P53; UNKNOWN_1.
SQ		SEQUENCE 590 AA.; 64725 MR.; 8580C7EFA21B5797 CRC64;		
Query		Match 83.6%; Score 2830.5%; DB 11; Length 590;		
Best Local Similarity 91.7%; Pred. No. 5, 8e-226;		Matches 531; Conservative 19; Mismatches 22;		Indels 7; Gaps 4;
Db	54	-MAQFNLLSAMDQGSRAPASPTPEAASAPTHSYQASSTFTMSAPVPSNTD 120.	QY 61	YMAQFNLLSAMDQGSRAPASPTPEAASAPTHSYQASSTFTMSAPVPSNTD 120.
Db	121	YQPHIFEVYEQSSSTPEHLNSLEPDTIFDLPSPGTSEAPSSEASQSEESNMDYFLQG-----	QY 121	YQPHIFEVYEQSSSTPEHLNSLEPDTIFDLPSPGTSEAPSSEASQSEESNMDYFLQG-----
Db	113	YQPHIFEVYEQSSSTPEHLNSLEPDTIFDLPSPGTSEAPSSEASQSEESNMDYFLQG-----	QY 181	YKAEHYTDYKRCPNHELGRENDEQOSAPASHLIREVGNMISQYDDPVTGRQSYVVPY 240
Db	173	YKAEHYTDYKRCPNHELGRENDEQOSAPASHLIREVGNMISQYDDPVTGRQSYVVPY 232	QY 241	EPQVGTTEFTILYFNMCNSCVGMMNRPLILITLEMRDQVLGRSSEGRICACPGR 300
Db	233	EPQVGTTEFTILYFNMCNSCVGMMNRPLILITLEMRDQVLGRSSEGRICACPGR 292	QY 233	DRKADEDHYREQQALNESSKNGASKRAFKQSPAPVALGAVKERRHGDFTYLYQVR 360
Db	293	DRKADEDHYREQQALNESSKNGASKRAFKQSPAPVALGAVKERRHGDFTYLYQVR 352	QY 361	GREENFELTMKIKESLLEMVLYPQLDVSYR--QQQQLQLRQSHLQPSYGVLSPLANKVH 418
Db	353	GREENFELTMKIKESLLEMVLYPQLDVSYRQQQQQLQLRQSHLQPSYGVLSPLANKVH 412	QY 419	GGNNKLPSVNVOLYQOPPHSSAATPNLGFYGPGLMNNHGHAYPANGEMSSAHSQAOSMVSG 478
Db	413	GGNNKLPSVNVOLYQOPPHSSAAGPNLGMGSMLNSHGSAPANGMNGHSSQMVSG 472	QY 479	SHCTPPPPYHADPSLYSETGLGPNCIEFTSGQSLQYHQLNLTIEDGALKIPEQYR 538
Db	473	SHCTPPPPYHADPSLYSETGLGPNCIEFTSGQSLQYHQLNLTIEDGALKIPEQYR 532	QY 539	MIIWRLQDLKQGHDYSTAQOLLR-SSNATISIGGSELQRYMEAVERVTTITP 597
Db	533	MIIWRLQDLKQSHD--CGQOLRISSSNATISIGGSELQRYMEAVERVTTITP 590	QY 598	NRGGPGG - GDEWADFGFLPDKARKOPIKEEFTEAIEH 636
Db	591	NRGGAGAVTGDEWADFGFLPDKSRKOPIKEEFTETESH 631	QY 591	NRGGAGAVTGDEWADFGFLPDKSRKOPIKEEFTETESH 631
RESULT 2	Q9JJP1	PRELIMINARY; PRT; 590 AA.	Q9JJP1	PRELIMINARY; PRT; 590 AA.
AC	Q9JJP1;		AC	Q9CUT7; PRELIMINARY; PRT; 514 AA.
DT	01-OCT-2000 (TRIMBrel. 15, Created)		DT	01-JUN-2001 (TRIMBrel. 17, Created)
DT	01-OCT-2000 (TRIMBrel. 15, Last sequence update)		DT	01-JUN-2001 (TRIMBrel. 17, Last sequence update)
DT	01-DEC-2001 (TRIMBrel. 19, Last annotation update)		DT	01-DEC-2001 (TRIMBrel. 19, Last annotation update)
DE	P73 DELTA-N PROTEIN.		DE	DE TRANSFORMATION RELATED PROTEIN 73 (FRAGMENT).
GN	TRP73 OR P73.		GN	GN TRP73.
OS	Mus musculus (Mouse).		OS	OS Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		OC	
OX	NCBI_TaxID:10090;		OX	OX NCBI_TaxID:10090;
RN	SEQUENCE FROM N.A.		RN	RN SEQUENCE FROM N.A.
RX	MEDLINE=20179195; PubMed=10716451;		RC	RC STRAIN=C57BL/6J; TISSUE=HEAD;
DR	Y19235; CAB81954.1;		DR	DR MEDLINE=2108560; PubMed=1217851;
DR	HSSP; 015330; C1OK		DR	RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
DR	MGI:1336919; Trp7.		DR	RA Arakawa K., Iizuka M., Nishi K., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
DR	InterPro; IPR02117; Trp7.		DR	RA Aizawa K., Iizuka M., Nishi K., Fukunishi Y., Konno H., Fondo S., Yamamoto I.,
DR	InterPro; IPR01660; SAM.		DR	RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
DR	Pfam; PF00870; P53; 1.		DR	RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
DR	Pfam; PF00336; SAM; 1.		DR	RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
PRINTS; PRO0386; P53UPPRESSR.				

Db	467	MGTH--MPPAGDMMGLSPQALPPPLSMPSHTSHCTPPPPYTDCTSVSFLARLGSSCL	523	QY	103	SSTFDIMSPAPVIPSNTDYPGPPIQHFEVTFOQSSATAWTSPLKKLYCQIAKTCPIQ	162	
QY	507	EYFTSQGLQSTIYHQLNLTEDLGALKIPEQYRATIWLQDJKQHDYSTAQQLRS-SN	565	Db	153	SSTFDALSPPAISNTDYPGPPISEDYSFQQSSTARATWTSPLKKLYCQIAKTCPIQ	212	
Db	524	DYFTTQGLTTRYQTEHYSHMDLASICUKIPEQFRHAIWKGILDRQHEFSSPHLRLTPSS	583	QY	163	IKVSTTEPPGTAIRAMPYKKAHRVTDVVKCPNHELGDRNEGOSAPASHLIRVEGNNL	222	
QY	566	ATATISGGGGLQLQRORVMEMAVHFRVRRHTTIPURGGPQEGPDAEGFDLPIKARKQD	625	Db	213	IKVMTTPPQGAVIRAMPYKKAHRVTEVKCPNHELSRENEQGIAFPASHLIRVEGNSH	272	
Db	584	ASTVSV-GSSETRGERVIDAVRFLRQTISFPPR-----DEWNDFNDARRNQQR	635	QY	223	SOYDDPVTGROSIVVYYPEQYGEFTTILYNEWMCNISCVGGMNRRLILITLLEMRDG	282	
QY	626	IKEE 629		Db	273	AQYDPIGQSVLPYEPQGTEFTTIVLNFMCNISCVGGMNRPLILITLLETRDG	332	
Db	636	IKEE 639		QY	283	QVLGRSFEGRICACPGDRKADEDHYREQQALNESSAKNGAASKRAFKOSPPAYPALGA	342	
RESULT 7				Db	333	QVLTGRICFERRACPGDRKADEDSSIRKQV - SDSTKNGDTRKPRFRONTHGQIM - T	388	
Q9H3D4		PRELIMINARY;	PRT;	680 AA.	QY	397	397	
AC	Q9H3D4				Db	389	GVKKRRHGDDEDTYLYQVRGRBENFILMLIKESTELMLVPLQPLDVSYRQQQ-----M	452
DT	01-MAR-2001	(TRIMBLrel. 16, Created)			QY	398	RPSHLO-PPSTICGPVILSPANKVHGMNKLPSVNLQYGPPISSAATPNLGPVGP-----M	452
DT	01-MAR-2001	(TRIMBLrel. 16, Last sequence update)			Db	449	KOTSIQSPSTYGNSSPLAKMN - SMNKLPSVQLIN - POORNALPTPTIPDGKANTIM	505
DT	01-DEC-2001	(TRIMBLrel. 19, Last annotation update)			QY	453	LNNHGHAYPANGMSSHSQ-----SVAVSGSHCTPPPPHADPSLVSEFTGLCPNCI	506
TA	P63	ALPHA.			Db	506	MGTH--MPPAGDMNGLSPQALPPLSMPSHTSHCTPPPPVPTDCSIVSFLARLGSSCL	562
OS	Homo sapiens (Human)				QY	507	EYFTSQGLOSIYHQLNLTIDGLALKIPEQYRMTIWGLDJKQHDYSTAQQLRS-SN	565
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Db	563	DIFTTQQLTIVQIEHYSMDLASKIPIKQFHRWKGLDHRQHEFSSPSHLLRTPSS	622
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;				QY	566	ARTISIIGSGELQYQRMVMEVHFYRHTHITIPQRGGPQGPDEWADEFGFDPDCARKOP	625
RN	[1]				Db	623	ASVSV-GSSETRGERVIDAVRFLRQTISFPPR-----DEWNDFNDARRNQQR	674
GN					QY	626	IKEE 629	
RP	SEQUENCE FROM N.A.				Db	675	IKEE 678	
RA	Hagiwara K., McMenamin M.G., Harris C.C.;				RESULT 8			
RA	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.				Q994E3	PRELIMINARY;		
RL					ID	Q994E3	PRELIMINARY;	
DR	EMBL; AF124539; AAG45607..1;				AC	Q994E3	PRELIMINARY;	
DR	EMBL; AAG45607..1;				DT	01-JUN-2001	(TRIMBLrel. 17, Created)	
DR	EMBL; AF124539; AAG45607..1;				DT	01-JUN-2001	(TRIMBLrel. 17, Last sequence update)	
DR	EMBL; AF124539; AAG45607..1;				DT	01-DEC-2001	(TRIMBLrel. 19, Last annotation update)	
DR	EMBL; AF124539; AAG45607..1;				DE	TA1	KET ALPHA PROTEIN.	
DR	EMBL; AF124539; AAG45607..1;				GN	P63		
DR	EMBL; AF124539; AAG45607..1;				OS	Rattus norvegicus (Rat).		
DR	EMBL; AF124539; AAG45607..1;				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DR	EMBL; AF124539; AAG45607..1;				OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
DR	EMBL; AF124539; AAG45607..1;				NCBI_TAXID	10116;		
DR	EMBL; AF124539; AAG45607..1;				RN	[1]		
DR	EMBL; AF124539; AAG45607..1;				RP	SEQUENCE FROM N.A.		
DR	EMBL; AF124539; AAG45607..1;				RC	STRAIN-NISTAR; TISSUE-TONGUE;		
DR	EMBL; AF124539; AAG45607..1;				RX	MEDLINE=21363378; Published-11470269;		
DR	EMBL; AF124539; AAG45607..1;				RA	"Identifier and tissue distribution of novel KET/p63 splice variants";		
DR	EMBL; AF124539; AAG45607..1;				RT	FEBS Lett. 501:121-126(2001).		
DR	EMBL; AF124539; AAG45607..1;				RL	EMBL; AJ77446; CAC37098..1; -.		
DR	EMBL; AF124539; AAG45607..1;				DR	HSSP; P04637; 1YCS.		
DR	EMBL; AF124539; AAG45607..1;				DR	InterPro; IPR02117; P53.		
DR	EMBL; AF124539; AAG45607..1;				DR	InterPro; IPR01650; SAM.		
DR	EMBL; AF124539; AAG45607..1;				DR	Pfam; PF00870; P53..1.		
DR	EMBL; AF124539; AAG45607..1;				DR	PRINTS; PR00386; P53..1.		
DR	EMBL; AF124539; AAG45607..1;				DR	ProDom; PD00281; P53..1.		
DR	EMBL; AF124539; AAG45607..1;				DR	SMART; SM00454; SAM..1.		
DR	EMBL; AF124539; AAG45607..1;				DR	PROSITE; PS000448; P53..1.		
DR	EMBL; AF124539; AAG45607..1;				DR	SEQUENCE 663 AA; 74660 MW; C953BBAC389D5B70 CRC64;		
DR	EMBL; AF124539; AAG45607..1;				SQ	93 MDCTRMQDSLSDMNPWQYTNLGNMSDQIQNGSSSTSYNTDHAQNSVTAPSPYQD	152	

Query Match	52.9%; score 1789; DB 11; Length 663;	RL Mol. Cell 2:305-316(1998); DR AF075436; AAC2641.1; DR HSSP; P04637; 1YCS.
Best Local Similarity	55.1%; Pred. No.:1.4e-39;	DR MGI:1330810; TRP63;
Matches	93; Mismatches 145; Indels 60; Gaps 18;	DR InterPro; IPR002117; P53.
Qy	1 MAOSTAT--SPDGTTTFBLLWSSL--DSTYFDIPOSSRGNNEVGTDSS 48	DR InterPro; IPR001660; SAM, Pfam; PF00810; P53; 1.
Db	23 MSQSTQNSEFLSPE--VFIQHIDFLEQPCSYQPIDLNFIYDPESENGATNKI---EIS 75	DR PRO386; P53; PRESSR.
Qy	49 MDVPHLEGMTS---VMAQFNLLSSTDQMSRASAASPTPEHA-SYTHSPYAQ 102	DR PRO02681; P53; 1.
Db	76 MDICRQDSLSDPMPQPYQYQNLGLINGDQIQNSSTSPTYDQHONSTAPSPYAQ 135	DR SMRT; SM00454; SAM; 1.
Qy	103 SSTDFTMSPAVPIVSTDYPGSPHHEFTFQQSSTAKSATWTTSPLLKLYCQIAKTCPIQ 162	DR SEQUENCE 680 AA; 76788 MW; BDEF0284F247C68A CRC64;
Db	136 SSTDFTMSPAVPIVSTDYPGSPHHEFTFQQSSTAKSATWTTSPLLKLYCQIAKTCPIQ 195	Query Match 52.9%; Score 1789; DB 11; Length 660; Best Local Similarity 55.1%; Pred. No.:1.4e-19; Mismatches 94; Indels 60; Gaps 18; Matches 366; Conservative 94; Mi matches 144; DR 40 MSQSTQNSEFLSPE--VFIQHIDFLEQPCSYQPIBLNFYDEPSENGAINKI---EIS 92
Qy	163 IKVSTPPPPGTAIRAMPVYKKAERHTDVKRCPNHELGDRDNEGQASPHSLIRVEGNL 222	QY 1 MAQSTAT---SPDGTTTFBLLWSSL--DSTYFDIPOSSRGNNEVGTDSS 48
Db	196 IKVMTTPPQGAVYIRAMPVYKKAERHTEVVKRCPNHELSRFNEQIAPPSPHSLIRVEGNH 255	QY 1 MAQSTAT---SPDGTTTFBLLWSSL--DSTYFDIPOSSRGNNEVGTDSS 48
Qy	223 SQTYDPTVIGRSVYPPYEPQVGYGEEFTLYNFMNCNSCCGMRNMRPILITLLEMRDG 282	QY 49 MDVPHLEGMTS---VMAQFNLLSSTDQMSRASAASPTPEHA-SYTHSPYAQ 102
Db	256 AQIVEDITGROSVLVYEPQVGYGEEFTLYNFMNCNSCCGMRNMRPILITLLEMRDG 315	QY 49 MDVPHLEGMTS---VMAQFNLLSSTDQMSRASAASPTPEHA-SYTHSPYAQ 102
Qy	283 QVIGRRSFEGRTICACPGDRKADEDHYREQOALNESSAKNGASAKRAFKOSPPAVPALA 342	Db 93 MDCIRQDSLSDPMPQTYDQHONSTAPSPYAQ 152
Db	316 QVIGRRCFEEARICACPGDRKADEDSTIKRQV--SDSARNGDGTKRFQONTGIM-T 371	QY 103 SSTDFTMSPAVPIVSTDYPGSPHHEFTFQQSSTAKSATWTTSPLLKLYCQIAKTCPIQ 162
Qy	343 GYKKRRHGDDETYLQYQRGRENFEILMLKLESLEMLMVLQYPLVDYSRQQQ---LLQ 397	Db 153 SSTDFTMSPAVPIVSTDYPGSPHHEFTFQQSSTAKSATWTTSPLLKLYCQIAKTCPIQ 212
Db	372 SIKKRRSPDDELLYLPVRGTRYEYMLKLESLEMLQYLPVORTIETYRQQQQHQHLLQ 431	QY 163 IKVSTPPPPGTAIRAMPVYKKAERHTDVKRCPNHELGDRDNEGQASPHSLIRVEGNL 222
Qy	398 RPSHILQ-PPSHPVLPSPMVNHGANKLPSVNLQVQPPPHSSAATPNLPGVPG---M 452	Db 213 IKVMTTPPQGAVYIRAMPVYKKAERHTEVVKRCPNHELSRFNEQIAPPSPHSLIRVEGNH 272
Db	432 KOTSMOSQSYGNSSPPLNCKN-SHANKLPSVSQLIN--PQRNAVLTPTMPEGMGANIPM 488	QY 223 SQTYDPTVIGRSVYPPYEPQVGYGEEFTLYNFMNCNSCCGMRNMRPILITLLEMRDG 282
Qy	453 LANNHGHAVPANGEMSSHSQ---SAYSGSICSTPPPPYHADPSLVSFLTGGLCPNCI 506	Db 273 AQYVEDITGROSVLVYEPQVGYGEEFTLYNFMNCNSCCGMRNMRPILITLLEMRDG 332
Db	489 MGTTH---MPMAGDMNLSPQALPPPLSWSSTSUICTPPPYPPDCS1TYSFARLGSSCL 545	QY 283 QVIGRRCFEEARICACPGDRKADEDHYREQOALNESSAKNGASAKRAFKOSPPAVPALA 342
Qy	507 EYFTSQGLOSTYHQLNQTSITDGLALKIPEGYRATIWRGQDQDQKGDYSTAQQLRS-SN 565	Db 333 QVIGRRCFEEARICACPGDRKADEDSTIKRQV--SDRANKGDTKRFQONTGIM-T 368
Db	546 DIFTTQGSLITTYQIERYSMDDLASUKIPECFRHAWKGLDARQLHDESSPHLLRTPSG 605	QY 343 GYKKRRHGDDETYLQYQRGRENFEILMLKLESLEMLMVLQYPLVDYSRQQQ---LLQ 397
Qy	566 AATISIGSGELQQRVMEAVFVRYRHTITIPNRGGPGGGDWEADFGFDLPDCKARKOP 625	Db 389 SIKKRRSPDDELLYLPVRGTRYEMLKLESLEMLQYLPVORTIETYRQQQQHQHLLQ 448
Db	606 ASTVSV GSSETRGERVIDAVRFLRQTISFPPR-----DEWNDFNDDMSRRNKKQR 657	QY 398 RPSHILQ-PPSHPVLPSPMVNHGANKLPSVNLQVQPPPHSSAATPNLPGVPG---M 452
Qy	626 TIEE 629	Db 449 KOTSMOSQSYGNSSPPLNCKN-SHANKLPSVSQLIN--PQRNAVLTPTMPEGMGANIPM 505
Db	658 IKEE 661	QY 453 LNNHGHAVPANGEMSSHSQ---SMVSGSHCTPPPPYHADPSLVSFLTGGLCPNCI 506
RESULT 9		Db 506 NGTH--MPMAGDMNLSPQALPPPLSWSSTSUICTPPPYPPDCS1TYSFARLGSSCL 562
Q88898	PRELIMINARY; PRT; 680 AA.	QY 507 EYFTSQGLOSTYHQLNQTSITDGLALKIPEGYRATIWRGQDQDQKGDYSTAQQLRS-SN 565
AC	088898; PRELIMINARY; PRT; 680 AA.	Db 563 DYFTTQGSLITTYQIERYSMDDLASUKIPECFRHAWKGLDARQLHDESSPHLLRTPSG 622
DT	01-NOV-1998 (TREMBLrel. 08, Created)	QY 566 ANTISIGSGELQQRVMEAVFVRYRHTITIPNRGGPGGGDWEADFGFDLPDCKARKOP 625
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	Db 623 ASTVSV GSSETRGERVIDAVRFLRQTISFPPR-----DEWNDFNDDMSRRNKKQR 674
DE	1AP63 ALPHA.	QY 626 IKEE 629
GN	TRP63.	Db 675 IKEE 678
OS	Mus musculus (Mouse)	RESULT 10
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Q9JJP6
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	ID Q9JJP6; PRELIMINARY; PRT; 680 AA.
RN	[1]_	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	AC Q9JJP6; PRELIMINARY; PRT; 680 AA.
RX	MEDLINE-98448095; PubMed-974969;	DR 01-OCT-2000 (TREMBLrel. 15, Created)
RA	Yang A., Kachad M., Gillert E., Fleming M.D., Dotsch V., Andrews N.C., Capet D., McKeon F.;	DR 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
RA	"P63, a P53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities";	DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
RT		TAZ KET ALPHA.

Db	114	SSTFDALSPSPAIAPSNTDYPGPHSFDVFSQQSSAKSATWYSTELKKLYCQIAKTCPIQ	173	Qy	1	MAQSTAT----SPGGGTTTERRLASSLP-----DSTFDLPOSSENNEVGGDSS-48	
Qy	163	IKVSTDPPTPDAIRAMPYKKAERHTDVVKRCPNHELGDRDNEQQSAPASHLIRVEGNL	222	Db	40	MSQSQTNTFNLSPB----VFOHQHIDFELQEPICSVQPIDLNVEDESEGDATNKI----EIS-92	
Db	174	IKVMPDPPQGAVIRAMPYKKAERHTEVVKRCPNHELGDRDNEQQIAPPShLIRVEGNSh	233	Qy	49	MDVFHLEGMTS----YMAQFQULLSTMDOMMSRASASPPYTPHAA-SVPHSPYQAQ	
Qy	223	SQYVDDPVTRGOSVTPYBPQVGETFETILYLNFMCNSSCYGGMNRPLILITLLEMRDG	282	Db	93	MDCTEMQDSDLSBDMPTQYTNGLINEMDQIQQSSSTSPYNTDHAQNSVTPSPYTAQP	
Db	234	AQYVEPPTGROSVLPVYEPPOVGETFETILYLNFMCNSSCYGGMNRPLILITLLEMRDG	293	Qy	103	SSTFDLSSPAVIPSNTDYPGPHFEVTFQOSSTAKSATWYSTSPYNTDHAQNSVTPSPYTAQP	
Qy	283	QVLGRRSFEGRICACPGDRKADEDHYREQUALNESSAKNGAASKRAFKFOSPPAVPALGA	342	Db	153	SSTFDALSSPAVIPSNTDYPGHSFDVSFQSOSSTAKSATWYSTSPYNTDHAQNSVTPSPYTAQP	
Db	294	QVLGRRCFEERICACPGDRKADEDSTIKRQV--SDSTKNGDTKRPFRONTHGQM--T	349	Qy	163	IKVSPPPPCTAIRAMPYKKAERHTDVVKRCPNHELGDRDNEQOSAPASHLIRVEGNL	
Qy	343	GYKRRHGDDDTYLQYRGENFILMLKIKSEELMELVPLDYSYRQQQ----LLQ	397	Db	213	IKVMPDPPGAVIRAMPYKKAERHTEVVKRCPNHELSRFSPNEQIAPPShLIRVEGNSh	
Db	350	SIKKRSRSPDDELLPVRERETYMLKIKSEELMELVPLDYSYRQQQOOHOHLLQ	409	Qy	223	SQYVDPYVNGROSYVPPYEPPOVGETFETILYLNFMCNSSCYGGMNRPLILITLLEMRDG	
Qy	398	RPSHILQ-PPSYGPVLPSPMKVHGMNMKLPSPVNLQYGPQPHPSAATPNLGPVGPQ----M	452	Db	273	AQYDPDPTGQSYLVPYEPPOVGETFETILYLNFMCNSSCYGGMNRPLILITLLEMRDG	
Db	410	KOTSTQSPSYGNSSPPLAKMN-SMNKLPSPVOLIN--PQRNALPTPTIPDGNGANTIM	466	Qy	283	QVLGRRSFEGRICACPGDRKADEDHYREQUALNESSAKNGAASKRAFKFOSPPAVPALGA	
Qy	453	LNNHGHAVPANGEMSSSHSAQ----SMVGSHTCPTPPPHADPSLVSITLGUCPNCI	506	Db	333	QVLGRRCFEERICACPGDRKADEDSTIKRQV--SDSTKNGDTKRPFRONTHGQM--T	
Db	467	NGTH--MPAGADMGLSPTQALPPLPSMPSHTSHCPTPPPPPTDCSIVGTLARLGCSCL	523	Qy	343	GVKKERHGGDDEDTYLQVRGRENFEILMKLKSLELMELVPLDYSYRQQQ----LLQ	
Qy	507	EYFTSGQLQIYHQLNLTEDGALKIPEQYRATIWGLQDQKGIDYSTAQQLRS--SN	565	Db	389	SIKKRSRSPDDELLPVRERETYMLKIKSEELMELVPLDYSYRQQQOOHOHLLQ	
Db	524	DYFTQGLQTLTYQIEHYSDNLASLKIPEQFHAIKGTLHRLHEFSSPHLRTTPS	583	Qy	398	RPSHILQ-PPSYGPVLPSPMKVHGMNMKLPSPVNLQYGPQPHPSAATPNLGPVGPQ----M	
Qy	566	AATISGGSSELQFORMEAVERVRHTITIPNRRGGGGPDEWADFGFLDCKARKOP	625	Db	449	KQTSTQSPSYGNSSPPLAKMN-SMNKLPSPVOLIN--PQRNALPTPTIPDGNGANIPM	
Db	584	ASTVSY-GSSETRSERVIDAVRPTLRTQFISPFPR----DEWDNFNDMARDNKKQR	635	Qy	453	LNNHGHAVPANGEMSSSHSAQ----SMVGSHTCPTPPPHADPSLVSITLGUCPNCI	
Qy	626	IKEE 629		Db	506	MGTH--MPAGADMGLSPTQALPPLPSMPSHTSHCPTPPPPPTDCSIVGTLARLGCSCL	
Db	636	IKEE 639		Qy	507	EYFTSQGLQIYHQLNLTEDGALKIPEQYRATIWGLQDQKGIDYSTAQQLRS--SN	
RESULT 12							
Q9UE10		PRELIMINARY;		Db	563	DYFTQGLQIYHQLNLTEDGALKIPEQYRATIWGLQDQKGIDYSTAQQLRS--SN	
ID	Q9UE10			Qy	566	AATISGGSSELQFORMEAVERVRHTITIPNRRGGGGPDEWADFGFLDCKARKOP	
AC	Q9UE10;	PRELIMINARY;		Db	623	MGTH--MPAGADMGLSPTQALPPLPSMPSHTSHCPTPPPPPTDCSIVGTLARLGCSCL	
DT	01-MAY-2000 (TREMBLrel. 13, Created)			Qy	626	ASTVSY-GSSETRSERVIDAVRPTLRTQFISPFPR----DEWDNFNDMARDNKKQR	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			Db	675	IKEE 678	
DE	KET. PROTEIN.			RESULT 13			
GN	KET.			089097	PRELIMINARY;	PRT;	586 AA.
OS	Homo sapiens (Human)			TD	089097;		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			AC	089097;		
OC	Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo;			DT	01-NOV-1998 (TREMBLrel.		
OX	NCBI-TAXID=9600;			DT	01-NOV-1998 (TREMBLrel.		
RN	[1]			DT	01-JUN-2001 (TREMBLrel.		
SEQUENCE FROM N.A.				DT	01-JUN-2001 (TREMBLrel.		
RC	SEQUENCE FROM N.A.			DE	DN P63 ALPHA.		
RX	RC TISSUES: SKELETON, MUSCLE AND KERATINOCYTE CULTURE;			GN	TRP63 OR P73H.		
RX	MEDLINE-95018235; PubMed-979841;			OS	Mus musculus (Mouse).		
RA	Augustin M., Bamberger C., Paul D., Schmale H;			OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RA	*Cloning and chromosomal mapping of the human p53-related KET gene to			OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
RT	chromosome 3q27 and its murine homolog KET to mouse chromosome 16."			OX	NCBI_TaxID=10090;		
RL	RL Mamm. Genome 9: 899-902(1998).			RN	SEQUENCE FROM N.A.		
DR	DR EMBL: Y16361; CAA70562.1; -			RP	SEQUENCE FROM N.A. PubMed=974969;		
DR	DR HSSP; P04637; YICS.			RX	MEDLINE-38448095;		
DR	DR InterPro: IPR021117; P53.			RA	Yang A., Kaghad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,		
DR	DR Pfam: PF00870; P53_1.			RA	Caput D., McKeon F.;		
DR	DR PRODOM; PR00386; P53SUPPRESSR.			RA	*P63, a P53 homolog, encodes multiple products with		
DR	DR SMART; SM00454; SAM; 1.			RT	"transactivating, death-inducing, and dominant-negative activities";		
SQ	SEQUENCE 680 AA; 6548AF2187D855E CRC64;			RL	RT transactivating, death-inducing, and dominant-negative activities";		
Query Match 52.7% Score 1782 DB 4; Length 680;				RN	RL Mol. Cell 2:305-316(1998).		
Best Local Similarity 55.0% Pred. No. 5.3e-139; Mismatches 145; Indels 60; Gaps 18;				RN	[2] SEQUENCE FROM N.A.		
Matches 365; Conservative 94; Gaps 18;				RP			

Db	377_SMRNLPSYTSQLIN- -PQRNALTPPTIPDGNGANPPMGTH-- -MMAGDMNGNLSPQAL 431	Db	300_RSPDDELLYLVGRGTYEMILKJIKESLELMQYDQHTBTYQQQQQQHQHLLQKOTSM 359
Qy	474 ---SMVSGSHCTPPYHADPSLYFLTGJGCPNCTEYTSQGLQSTYHQLNLTEDLG 529	Qy	403_Q-PPSYGVLPSPMKYVHGMMKLPSPSYNQLYGQPSPHSSATPNTGPGPGP---MLNNHG 457
Db	432_PPPISMPPTSHCTPPYHADPSLYFLTGJGCPNCTEYTSQGLQSTYHQLNLTEDLG 491	Db	360_QSOSYGNSSPPNKKN-SNANKLPSYTSQLIN- -DQQRNALTPTMPGNGANTIPMGTH- 415
Qy	530_ALK1PEQRMTIWRGLQDLCGHDYSTAQQCLRS_SNAATISIGGSGELQRQRYMEAVHF 588	Qy	458_HAYPANGEMSSHSQA --- SMVSGSHCTPPYHADPSLYFLTGJGCPNCTEYTSQGLQSTYHQLNLTEDLG 511
Db	492_SLK1PEQRHAWKGQDHLRQHESFSPSHLRTSSASVSV_SGSSTRGERVIDAYRF 550	Db	416 -APMAGDMNGLSPPTQALPPLSPMSPTSHCTPPYHADPSLYFLTGJGCPNCTEYTSQGLQSTYHQLNLTEDLG 473
Qy	589_RYRHTITIPNRCGPGGGPDEADFGSDLPCKARQKPIKE 639	Qy	512_QGLOSITHLQNLTIEDGALK1PEQRMTIWRGLQDLCGHDYSTAQQCLRS_SNAATISIGGSGELQRQRYMEAVHF 570
Db	551_TLRQTSFPPR-----DERNDFNDMARRNKQKRIKE 584	Db	474_QGLTTTQIEHYSMDDLASLKIPEQFRHAWKGQDHLRQHESFSPSHLRTSSASVSV_SGSSTRGERVIDAYRF 533
Qy	590_RYRHTITIPNRCGPGGGPDEADFGSDLPCKARQKPIKE 629	Qy	571_IGGGELORQRYMEAVHFRVHTTIPNRCGPGGGPDEADFGSDLPCKARQKPIKE 629
Db	Q99JE2_PRELIMINARY; PRT: 586 AA.	Db	534_V-ESSETGERVTDVAFTRTQTSFPPR-----DERNDFNDMARRNKQKRIKE 584
AC			
DT	01-JUN-2001 (TREMBLrel. 17, Created)	Search completed: November 7, 2002, 10:12:27	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	Job time : 29.2727 secs	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	DN KET ALPHA PROTEIN_N		
GN			
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID:10116;		
RN			
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NISTAR; TISSUE-TONGUE;		
RX	MEDLINE=21363378; Published=11470269;		
RA	Bamberger C.; Schmale H.;		
RT	"Identification and tissue distribution of novel KET/p63 splice variants";		
RT	"Identification and tissue distribution of novel KET/p63 splice variants";		
RL	FEB5 Lett.; 501:126(2001).		
DR	EMBL: Au7277447; CAC37099.1;		
DR	HSSP; P04637; 1ycs;		
DR	Bamberger C.; Schmale H.;		
DR	InterPro; IPR002117; P53.		
DR	InterPro; IPR001660; SAM.		
DR	Pfam; PF00870; P53; 1.		
DR	PRINTS; PR00386; P53PPRCSR.		
DR	ProDom; PD002681; P53; 1.		
DR	SMART; SM00454; SAM; 1.		
DR	PROSITE; PS00348; P53; UNKNOWN_1.		
SQ	SEQUENCE 586 AA; 65732 MN; 78AB8CC4F52BA743-CRC64;		
	Query Match 51.4%; Score 1740; DB 11; Length 586;		
	Best Local Similarity 58.1%; Pred. No. 1..3e-135;		
	Matches 348; Conservative 86; Mismatches 121; Indels 44; Gaps 14;		
Qy	57_MTVSMAQFN-----LLSSTMDOMSSRASASPPYTPBHA-SVPPHSPYQAQPSSTFD 107		
Db	4_Leucine-rich repeat motif		
Qy	108_TMSPAVTPSNTDYPGPHHFEVTFQOSSTARSKATSSATVSPYDQNSVTPAQPSSSTFD 167		
Db	64_ALSPPAAPSNTDYPGPHSFDSFQQSSTSKATSSATVTPYSTELKKLXQCAKTCPIQKVST 123		
Qy	168_PPPGTATRAMPYKKEHYTDVVKRCPNAHGFNEGOSAPASHLJRVGNNLQYD 227		
Db	124_PPPGAVATRAMPYKKEHYTDVVKRCPNAHGFNEGOSAPASHLJRVGNNLQYD 243		
Qy	228_DPYTGROSVVYVPPYQGTEFTTLYNFMNCNSVCGMNRPLLITLEBDGVJLGR 287		
Db	184_DPTTGROSVVYVPPYQGTEFTTLYNFMNCNSVCGMNRPLLITLEBDGVJLGR 243		
Qy	288_RSFFGRICAPGRDRADEDHYRQDQALNESSAKNGAASKRFAQSPPAVPAIAGVYKKR 347		
Db	244_RCFFARICAPGRDRADEDYSRKQOV - SDSAKNGDGTKRPRQNTGQM - TSIKKR 299		
Qy	348_RHGDEDTYLQYRGRGENFEILMKLESLEMVYDPLVDSYR000-----LJOPSHI 402		